



RECEIVED

OCT 31 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> ENDO, Keiji et al.

<120> MUTANT ALPHA-AMYLASES

<130> 2173-0120P

<140> US 09/590,375

<141> 2000-06-09

<150> JP P1999-163569

<151> 1999-06-10

<160> 23

<210>1

<211>480

<212>PRT

<213>Bacillus sp. KSM-K38

<400>1

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
5 10 15
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30
Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205
Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240
Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255
Phe Val Val Gly Glu Tyr Trp Lys Asp Val Gly Ala Leu Glu Phe
260 265 270
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu

	275		280		285
Asn Tyr	Asn Phe Tyr Arg	Ala Ser Gln Gln Gly Gly	Ser Tyr Asp Met		
290		295	300		
Arg Asn	Ile Leu Arg Gly	Ser Leu Val Glu Ala His	Pro Met His Ala		
305		310	315		320
Val Thr	Phe Val Asp Asn His Asp Thr	Gln Pro Gly Glu Ser Leu Glu			
	325	330	335		
Ser Trp	Val Ala Asp Trp Phe Lys Pro	Leu Ala Tyr Ala Thr Ile Leu			
	340	345	350		
Thr Arg	Glu Gly Gly Tyr Pro Asn Val Phe Tyr	Gly Asp Tyr Tyr Gly			
	355	360	365		
Ile Pro	Asn Asp Asn Ile Ser Ala Lys Lys Asp	Met Ile Asp Glu Leu			
	370	375	380		
Leu Asp	Ala Arg Gln Asn Tyr Ala Tyr Gly Thr	Gln His Asp Tyr Phe			
385		390	395		400
Asp His	Trp Asp Val Val Gly Trp Thr Arg	Glu Gly Ser Ser Ser Arg			
	405	410	415		
Pro Asn	Ser Gly Leu Ala Thr Ile Met Ser	Asn Gly Pro Gly Gly Ser			
	420	425	430		
Lys Trp	Met Tyr Val Gly Arg Gln Asn Ala Gly	Gln Thr Trp Thr Asp			
	435	440	445		
Leu Thr	Gly Asn Asn Gly Ala Ser Val Thr Ile	Asn Gly Asp Gly Trp			
	450	455	460		
Gly Glu	Phe Phe Thr Asn Gly Gly Ser Val Ser	Val Tyr Val Asn Gln			
465		470	475		480

<210>2

<211>485

<212>PRT

<213>Bacillus sp. KSM-AP1378

<400>2

His His	Asn Gly Thr Asn Gly Thr Met Met	Gln Tyr Phe Glu Trp His			
	5	10	15		
Leu Pro	Asn Asp Gly Asn His Trp Asn Arg	Leu Arg Asp Asp Ala Ala			
	20	25	30		
Asn Leu	Lys Ser Lys Gly Ile Thr Ala Val Trp	Ile Pro Pro Ala Trp			
	35	40	45		
Lys Gly	Thr Ser Gln Asn Asp Val Gly Tyr Gly	Ala Tyr Asp Leu Tyr			
	50	55	60		
Asp Leu	Gly Glu Phe Asn Gln Lys Gly Thr Val	Arg Thr Lys Tyr Gly			
	65	70	75		80
Thr Arg	Ser Gln Leu Gln Gly Ala Val Thr Ser	Leu Lys Asn Asn Gly			
	85	90	95		
Ile Gln	Val Tyr Gly Asp Val Val Met Asn His	Lys Gly Gly Ala Asp			
	100	105	110		
Gly Thr	Glu Met Val Asn Ala Val Glu Val Asn	Arg Ser Asn Arg Asn			
	115	120	125		
Gln Glu	Ile Ser Gly Glu Tyr Thr Ile Glu Ala	Trp Thr Lys Phe Asp			
	130	135	140		
Phe Pro	Gly Arg Gly Asn Thr His Ser Asn Phe	Lys Trp Arg Trp Tyr			
	145	150	155		160
His Phe	Asp Gly Thr Asp Trp Asp Gln Ser Arg	Gln Leu Gln Asn Lys			
	165	170	175		
Ile Tyr	Lys Phe Arg Gly Thr Gly Lys Ala Trp	Asp Trp Glu Val Asp			
	180	185	190		

Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
 195 200 205
 Asp His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
 210 215 220
 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 225 230 235 240
 Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
 245 250 255
 Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 260 265 270
 Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
 275 280 285
 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
 290 295 300
 Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
 305 310 315 320
 His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335
 Gly Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala
 340 345 350
 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365
 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser
 370 375 380
 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr
 385 390 395 400
 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 405 410 415
 Gly Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430
 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly
 435 440 445
 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
 450 455 460
 Asn Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser
 465 470 475 480
 Val Trp Val Lys Gln
 485

<210> 3
 <211> 1753
 <212> DNA
 <213> Bacillus sp. KSM-K38

<220>
 <221> sig_peptide
 <222> (162)..(224)

<220>
 <221> mat_peptide
 <222> (225)..()

<220>
 <221> CDS
 <222> (162)..(1664)

```

<400> 3
gtatgcgaaa cgatgcgcaa aactgcgcaa ctactagcac tcttcaggga ctaaaccacc 60
ttttttccaa aaatgacatc atataaacia atttgtctac caatcactat ttaaagctgt 120
ttatgatata tgtaagcggt atcattaaaa ggaggtatatt g atg aga aga tgg gta 176
Met Arg Arg Trp Val
-20

gta gca atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca 224
Val Ala Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala
-15 -10 -5 -1

gat gga ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa 272
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1 5 10 15

aac gac ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg 320
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

agt gat gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt 368
Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

aat agt cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta 416
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

gga gag ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag 464
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

gca cag ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat 512
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

gta tac gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg 560
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

gag gca gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat 608
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

att tca ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca 656
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

ggg cgt aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt 704
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

aat ggt gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc 752
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

```

ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat	800
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn	
180 185 190	
tat gat tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta	848
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val	
195 200 205	
caa gat gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat	896
Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp	
210 215 220	
ttg gat ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat	944
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr	
225 230 235 240	
aca tct gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta	992
Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu	
245 250 255	
ttt gtc gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt	1040
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe	
260 265 270	
tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt	1088
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu	
275 280 285	
aat tat aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg	1136
Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met	
290 295 300	
cgt aat att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca	1184
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala	
305 310 315 320	
gtt acg ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag	1232
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu	
325 330 335	
tca tgg gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg	1280
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu	
340 345 350	
acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg	1328
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly	
355 360 365	
att cct aac gat aac att tca gct aaa aaa gat atg att gat gag ctg	1376
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu	
370 375 380	
ctt gat gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt	1424
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe	
385 390 395 400	

gat cat tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga	1472
Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg	
405 410 415	
cct aat tca ggc ctt gcg act att atg tgc aat gga cct ggt ggt tcc	1520
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser	
420 425 430	
aag tgg atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat	1568
Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp	
435 440 445	
tta act ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg	1616
Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp	
450 455 460	
ggc gaa ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa	1664
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln	
465 470 475 480	
taacaaaaag ccttgagaag ggattcctcc ctaactcaag gctttcttta tgtcgcttag	1724
cttaacgctt ctacgacttt gaagcttta	1753
<210>4	
<211>480	
<212>PRT	
<213>Bacillus sp. KSM-K36	
<400>4	
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu	
5 10 15	
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Glu Ala Leu	
20 25 30	
Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu	
50 55 60	
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75 80	
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn	
85 90 95	
Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala Asp Phe Thr	
100 105 110	
Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg Trp Gln Asp	
115 120 125	
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Pro	
130 135 140	
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe	
145 150 155 160	
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Leu Phe Arg	
165 170 175	
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn	
180 185 190	
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val	
195 200 205	
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp	

210		215		220
Leu Asp Gly Tyr Arg	Leu Asp Ala Ile Lys His	Ile Pro Phe Trp Tyr		
225	230	235	240	
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu				
	245	250	255	
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe				
	260	265	270	
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu				
	275	280	285	
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met				
	290	295	300	
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala				
305	310	315	320	
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu				
	325	330	335	
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu				
	340	345	350	
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly				
	355	360	365	
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu				
	370	375	380	
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe				
385	390	395	400	
Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg				
	405	410	415	
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser				
	420	425	430	
Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp				
	435	440	445	
Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp				
	450	455	460	
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln				
465	470	475	480	

<210>5

<211>1625

<212>DNA

<213>Bacillus sp.KSM-K36

<220>

<221>sig_peptide

<222>(40)..(102)

<220>

<221>mat_peptide

<222>(103)..(1542)

<220>

<221>CDS

<222>(40)..(1542)

<400>5

atgatatatg taagcgttat cattaaaagg aggtatttg atg aaa aga tgg gta	54
gta gca atg ctg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca	102
gat ggc ttg aat gga acg atg atg cag tat tat gag tgg cat cta gag	150
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu	
1 5 10 15	

aat gat ggg caa cac tgg aat cgg ttg cat gat gat gcc gaa gct tta	198
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Glu Ala Leu	
20 25 30	
agt aat gcg ggt att aca gct att tgg ata ccc cca gcc tac aaa gga	246
Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
aat agt cag gct gat gtt ggg tat ggt gca tac gac ctt tat gat tta	294
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu	
50 55 60	
ggg gag ttt aat caa aaa ggt acc gtt cga acg aaa tac ggg aca aag	342
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75 80	
gct cag ctt gag cga gct ata ggg tcc cta aag tcg aat gat atc aat	390
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn	
85 90 95	
gtt tat ggg gat gtc gta atg aat cat aaa tta gga gct gat ttc acg	438
Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala Asp Phe Thr	
100 105 110	
gag gca gtg caa gct gtt caa gta aat cct tcg aac cgt tgg cag gat	486
Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg Trp Gln Asp	
115 120 125	
att tca ggt gtc tac acg att gat gca tgg acg gga ttt gac ttt cca	534
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Pro	
130 135 140	
ggg cgc aac aat gcc tat tcc gat ttt aaa tgg aga tgg ttc cat ttt	582
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe	
145 150 155 160	
aat ggc gtt gac tgg gat caa cgc tat caa gaa aac cat ctt ttt cgc	630
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Leu Phe Arg	
165 170 175	
ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aat ggt aat	678
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn	
180 185 190	
tat gac tat tta tta gga tcg aac att gac ttt agc cac cca gag gtt	726
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val	
195 200 205	
caa gag gaa tta aag gat tgg ggg agc tgg ttt acg gat gag cta gat	774
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp	
210 215 220	
tta gat ggg tat cga ttg gat gct att aag cat att cca ttc tgg tat	822
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr	
225 230 235 240	
acg tca gat tgg gtt agg cat cag cga agt gaa gca gac caa gat tta	870
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu	
245 250 255	
ttt gtc gta ggg gag tat tgg aag gat gac gta ggt gct ctc gaa ttt	918
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe	
260 265 270	
tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt ccg ctc	966
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu	
275 280 285	
aat tat aat ttt tac cgg gct tca aag caa ggc gga agc tat gat atg	1014
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met	
290 295 300	
cgt aat att tta cga gga tct tta gta gaa gca cat ccg att cat gca	1062
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala	
305 310 315 320	

gtt acg ttt gtt gat aat cat gat act cag cca gga gag tca tta gaa	1110
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu	
325 330 335	
tca tgg gtc gct gat tgg ttt aag cca ctt gct tat gcg aca atc ttg	1158
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu	
340 345 350	
acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gac tac tat ggg	1206
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly	
355 360 365	
att cct aac gat aac att tca gct aag aag gat atg att gat gag ttg	1254
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu	
370 375 380	
ctt gat gca cgt caa aat tac gca tat ggc aca caa cat gac tat ttt	1302
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe	
385 390 395 400	
gat cat tgg gat atc gtt gga tgg aca aga gaa ggt aca tcc tca cgt	1350
Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg	
405 410 415	
cct aat tcg ggt ctt gct act att atg tcc aat ggt cct gga gga tca	1398
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser	
420 425 430	
aaa tgg atg tac gta gga cag caa cat gca gga caa acg tgg aca gat	1446
Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp	
435 440 445	
tta act ggc aat cac gcg gcg tcg gtt acg att aat ggt gat ggc tgg	1494
Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp	
450 455 460	
ggc gaa ttc ttt aca aat gga gga tct gta tcc gtg tat gtg aac caa	1542
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln	
465 470 475 480	
taataaaaag ccttgagaag ggattcctcc ctaactcaag gctttcttta tgctgtttag	1602
ctcaacgcctt ctacgaagct tta	1625

<210>6

<211>30

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>6

atgatgcagt attttgagtg gcatttgga 30

<210>7

<211>33

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>7

tatgagtggc atttgccaaa cgacgggcag cat 33

<210>8

<211>33

<212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>8
 ccagcctaca aaggtagtag tcaggcggat gtt 33

 <210>9
 <211>21
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>9
 gcacagcttc aacgagctat t 21

 <210>10
 <211>21
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>10
 tttcgacttt ccagggcgta a 21

 <210>11
 <211>33
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>11
 catattttcc gctttcaaaa tacgaactgg aac 33

 <210>12
 <211>33
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>12
 aactggcgag tggatgatga gaacggtaat tat 33

 <210>13
 <211>25
 <212>DNA
 <213>Artificial Sequence

<220>
 <223> PCR Primer

 <400>13
 tggatgaaga gttcggtaat tatga 25

 <210>14
 <211>33
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>14
 aatatcgact ttagtcgtcc agaagtacaa gat 33

 <210>15
 <211>33
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>15
 agtcatccag aggtcgtaga tgagttgaag gat 33

 <210>16
 <211>33
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>16
 gttgactggg atgagcgcaa acaagaaaat cat 33

 <210>17
 <211>34
 <212>DNA
 <213>Artificial Sequence

 <220>
 <223> PCR Primer

 <400>17
 atttgccaaa tgacgggcag cattggaatc gggt 34

 <210>18
 <211>34
 <212>DNA
 <213>Artificial Sequence

 <220>

<223> PCR Primer

<400>18

aaccgattcc aatgctgccc gtcatttggc aaat 34

<210>19

<211>40

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>19

gggtcgacca gcacaagccg atggattgaa cggtagcatg 40

<210>20

<211>29

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>20

taaagctttt gttattgggtt cacgtacac 29

<210>21

<211>30

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>21

gagtcgacca gcacaagccc atcataatgg 30

<210>22

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>22

taaagcttca atttatattg g 21

<210>23

<211>27

<212>DNA

<213>Artificial Sequence

<220>

<223> PCR Primer

<400>23

ccagatctac ttaccatttt agagtca 27

B¹